

Copyright GenoScope - version 5.1.4.P5, 4/5/2003 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: April 15, 2003, 00:17:43 ; Search time 63.5538 seconds

{ without alignments } 7904.14 Million cell updates/sec

Title: US-09-001-737-7_COPY_15_1652

Perfect score: 1638

Sequence: 1 ATGGCAAAAGAATCAATTGAGAGATGGCTGGCATGGTGGAGCTCAT 60

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 411362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMBO.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMBO.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMBO.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMBO.seq:*

5: /cgn2_6/ptodata/1/ina/PCATUS_COMBO.seq:*

6: /cgn2_6/ptodata/1/ina/parcifles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	1034.4	5365	4	US-08-961-527-77		Sequence 77, Appl
2	1234.6	5365	4	US-09-134-001C-1868		Sequence 1868, Appl
3	589.8	36.0	1647	4	US-09-477-971-5	Sequence 5, Appl
4	589.8	36.0	4524	4	US-09-477-971-7	Sequence 7, Appl
5	543.4	33.2	2415	4	US-09-221-017B-895	Sequence 695, Appl
6	528.2	32.2	1838	3	US-08-470-260-7	Sequence 7, Appl
7	528.2	32.2	1838	3	US-08-471-491-7	Sequence 7, Appl
8	528.2	32.2	1838	3	US-08-466-662-7	Sequence 7, Appl
9	528.2	32.2	1838	3	US-08-475-817C-6	Sequence 6, Appl
10	496.2	30.3	2284	2	US-08-467-822-8	Sequence 26, Appl
11	496.2	30.3	2284	4	US-08-437-691-28	Sequence 28, Appl
12	496.2	30.3	2280	4	US-08-466-624B-28	Sequence 28, Appl
13	458.6	28.0	440375	4	US-08-955-555A-3	Sequence 3, Appl
14	458.6	28.0	441329	4	US-09-013-040A-2	Sequence 2, Appl
15	458.6	28.0	441329	4	US-09-013-040A-1	Sequence 1, Appl
16	456.8	27.3	1626	2	US-08-997-060-19	Sequence 159, APP
17	456.8	27.3	1626	4	US-09-095-825-159	Sequence 159, APP
18	446.8	27.3	1626	4	US-09-095-825-159	Sequence 159, APP
19	446.8	27.3	1626	4	US-09-095-825-159	Sequence 159, APP
20	446.8	27.3	1625	4	US-09-205-416-159	Sequence 159, APP
21	446.8	27.2	1569	2	US-08-997-302-113	Sequence 113, APP
22	446.8	27.2	1569	2	US-08-997-302-113	Sequence 113, APP
23	444.8	27.2	1569	4	US-09-093-825-113	Sequence 113, APP
24	444.8	27.2	1569	4	US-09-093-825-113	Sequence 113, APP
25	444.8	27.2	1569	4	US-09-0205-416-113	Sequence 113, APP
26	444.8	27.2	1620	2	US-08-741-755-10	Sequence 10, APP
27	416.6	25.4	1620	3	US-09-031-608-10	Sequence 10, APP

RESULT 1
US-08-961-527-77
Sequence 77, Application US/08961527

1

General Information:

APPLICANT: Charles Kunisch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 415/33
. OPERATING SYSTEM: MS-DOS version 6.2
. SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961.527

FILED DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:
LENGTH: 5305 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-961-527-77

Query Match 63.2%; Score 1034.4; DB 4; Length 5365;
Best Local Similarity 77.4%; Pred. No. 3.7e-95%;
Matches 1254; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

QY 1 ATGGCAAAAGAATCAATTGAGAGATGGCTGGCATGGTGGAGCTCAT 60
Db 278 ATGTCAAAGAAATTAATTCTAGAGCCGCTAGCCANGTGTGCTGAT 337

QY	241	ATGATATTCGCGGTGATGGGAGGACTACTGCACACATTGACACGGCATTGAT	300
Db	244	ATGAAATCGCTGGGGACGGTACACAGCACACTTTCAGCACATCATGATCG	303
QY	301	GGGACTAAAGAATGTGAGCAGGAGTGTACACATTGTTAGGCTTCAAGGATGAA	360
Db	304	GGAGCTTACAGATTCAGAGTGTACAGTGGGACAGTCTAGCTTAAAGGTGAA	423
QY	361	ACGCAACAGCACAGCTTGTAGGCTTAAAGGCTCATGAGTTCTAAAGGTGAA	423
Db	364	AAAGCAGTCCAGTGTGCTTATAGGGCTCATGAGTTCTAAAGGTGAA	423
QY	421	GGAGTATTCGCTGGGGACGGTACACATTGTTAGGCTTCAAGGATGAA	480
Db	424	ACAGAGTGGCAGTGGGACGGTACACATTGTTAGGCTTCAAGGATGAA	483
QY	481	TCAGAGCTATGGGGTGGGACGGTACACATTGTTAGGCTTCAAGGATGAA	540
Db	484	TCTGAGCAAGGATTAAGTAGTGTACAGTGGCCTATCATGAGTGGG	543
QY	541	ATGGAACAGACCTGAGCTGGTGTGAGGCACTTCGCAATTGACGGTGTGTTACCTTCCTCAA	600
Db	544	TTTAATCAGGATTTAGTGAAGTGTAGTGTAGGAAAGTCATTGATGCGGTTATCATCCAA	603
QY	601	TACATGGCAGGACAACTGAAATAATGGTGCAGCCTGAAACCCATTATTCATC	660
Db	604	TATGGTAACTGACTGAGTAAATGATGAGCTGGTAAAGCTTCTAGGAGTTCAA	660
QY	661	ACGATATAAAAGGTCAACATCCAAAGCATTGTCGAACTCTGGGATTCAGA	720
Db	664	ACGGATAAGAATTCATCATTCCAAAGTATTCCTCAAGTAACTGAGTGGTCAAG	723
QY	721	ACCAACGCTCATACATCATGATGGGAGCTTCTGGGACTCTGGGATTCAGTAA	780
Db	724	GCTGTCGACCAATTATGTTGTTGGGAGTGAAGGCTTCAAGTAA	783
QY	781	GTCMTGACAGATTCGTTGCTTCATGTTGTTGGAGTGAAGGCTTCAAGTAA	840
Db	784	GTTCATGACAGATTCGTTGCTTCATGTTGTTGGAGTGAAGGCTTCAAGTAA	843
QY	841	GATGCTGTTAAAGCTATCTGACACATGTTACAGTGTGACAGTAA	900
Db	844	GATCGAGCTAAAGCAAGTTGAGGACCTAGCAATTAACTGCTCAGCTACT	903
QY	901	GAGGATCTGGCTTGTGAAAGTGTACAGCTGGGAGCTTCAAGTAA	960
Db	904	GATGTTAGTTGAGCTTAAAGATGATGCTCTGTGATGCTTGTGAGCTTAA	963
QY	961	ATTACAGTTGATAGTAGTAGACAGTAACTGTTGAGGTTGAGGCTTCAAGTAA	1020
Db	964	GTGAACTGACTAAAGTCATACACAGCTGGTGTAGTGTAAATGTTCAAGTAA	1023
QY	1021	GCTAACCGTTTGTGATGAACTTGTGAAACACACTCTGACTTGTACCGT	1080
Db	1024	GATGCTGTTGGTCAATTAAAGCACAATTGTGAGAACGATTCAGTGTAA	1083
QY	1081	GAAGAACATCAAAACCTTGGCAAAATTGAGGAACTCTGACATGAA	1140
Db	1084	GAAGAACATCAAAACCTTGGCAAAATTGAGGAACTCTGACATGAA	1143
QY	1141	GGTCTCACAGCAGCAGCTTAAAGAATGAACTTCACATGAGGATCTTAAATGCT	1200
Db	1144	GGTGGGAGTAAAGCAGGCTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAA	1203
QY	1201	ACAGGGTACGCCCTGTGAGGAGTGTCTCTGGTGTGACGACACTTAAAGGT	1260
Db	1204	ACAGCTGGCGCGGGTGGGAGGATCTGCTGCTGTTGTTACTCGCTTAA	1263
QY	1261	ATGAAAGAATGCTGAGCTCTGACTGTGAGGGCGTGTGACTGAGGTTACATGCT	1320
Db	1264	TATCGAAAGTGTGAATTAAGCAGAAGTGTGAAACGGGTTATCTGCTA	1323

QY 424 GCTATGTCGGTGGCGCGAATGATCACGTC--TGAAGTGGAGATATC 480
 Db 427 GCGTGTCTCAGGTGGTGTACCTCTCGCTAACTCCGAAACGAGTAACTGATC 486
 QY 481 TCAGAGTATGACCGCTGCGCAACGAGGTTGATACCGAGAACTGAGATCTGAGT 540
 QY 487 GTGAGAGGAGTGGAGAACGCTGCGTAAAGAAGGGTTATACCGTGGAGCTCCGCGT 546
 QY 541 ATGAAACAGACTGAGTGTGGAGCATCAATTGCCCTGGTTACCGTGGAGCTCAA 600
 Db 547 CTGGAGGAGGACTGGAGCTGGTGGAGGTTACCGTGGAGCTCCGCGT 606
 QY 601 TACGGTCAGAGAACGAAATGGTGGCGAGCTGAAACCTTATTCCTTAATC 660
 Db 607 TACHTCTCATCACAGCGAACCTGCGAGTGGACTGGAAACGCCGTTACCTGCTG 666
 QY 661 AGCGATAAAAGCTCAACCTCAAGAGATTGCGACTACTGTGAGGAGTTTAA 720
 Db 667 GCTGACAGAAGAACTCCAACTCGGAAAGCTGCCGGTTCGGAGAGCTGCCAA 726
 QY 721 ACCAACGTCGTTACTGATTTGCGAGTGTGAGTGGACTCCACCCCT 780
 Db 727 GCAGGAAACCGCGCTGATCGTCGAGGAGTGAAGAGCGAGGCGCACTG 786
 QY 781 GTTGTGACAGAGATCGGGTACTTCATGTTGTTGTCACGGCAGGATTTG 840
 Db 787 GTGCTTACACCATCGGGCTGAGTGGCTGCGTGGTTAACGACCGGGCTCGG 846
 QY 841 GATGCTGTTAAAGCATCTGAAACGACATGTGTATTCAGTGTGTTACAGTATA 900
 Db 847 GATGCGCTGAAAGCTGCGAGATATGGCAACCTGACTGGTGTACCGTGTCT 906
 QY 901 GAGGATCTAGACTGTAAAGATGTCAGATGACGCCCTGGACAGGCTGCTAG 960
 Db 907 GRAGAGATCGTGTGGCTGAGCTGGAAACACCTGCTAGGCTAACGT 966
 QY 961 ATTACAGTGTAAAGATGACGACACTAATTTGTAAGGGTCAAGGTT 1020
 Db 967 GTTGTGATCACAAAGACACCACTACATGAGGGTGTGAGAGGCGACATC 1026
 QY 1021 GCTAACCGTTGACTGATTAATGCCAATGARCAACAACTCTGACTTGACCGT 1080
 Db 1027 CAGGGCGGTGTGTCAGATCGTCAGATCGTCAGGTTGAGAGCAACTCTGACTGAC 1086
 QY 1081 GAAACTACAAACATTTGGGAAATAGTGTGTTGAGGTTAACATGCTAAAGTGA 1140
 Db 1087 GAAAACTGGGAGCCGGTAGCAACTGGCGGGTGTGCACTTACAAAGTGGT 1146
 QY 1141 GCTCCACAGAGACAGCTTAAAGAATGAAACTCTGCAATTGAGATGCTTAATGCT 1200
 Db 1147 GCTGTCACGAACTGTGAAAGAAGAAGAACGGGTGAAATGCTGGCG 1206
 QY 1201 ACACGGCAGCCCTGTAGAGGATGCTGTTGGGACGACCTTATGGTT 1260
 Db 1207 ACCCGPGCGCCGCTAGAGGCGCTGAGTGGTGTGGTGTGGCTGATCCGCTA 1266
 QY 1261 ATTGAAAGATGACGAGCTGACTCTGAGGGGTGAGTGTGACTGAGTACA--TT 1317
 Db 1267 GCGTCATAACTGCTGACGGCTGCGGGTGTGAGGAGCTGTTACAGTT 1326
 QY 1318 GGCGCTCGGCTCTAGAGGCGCTGAGTGGTGTGGTGTGGCTGATCCGCTA 1377
 Db 1327 GCGCTCGGCGCAATGGAGCTCCCTCGTCGATGCGATGCGACG 1386
 QY 1378 TCGGAGTATGACGAGTGTGAAACGCGCTGAGGAGTTATGTTGACAA 1437
 Db 1387 TCTGTTGTTGCTACCGCTAAGGGCGACCGCACTAGGTACACCGAAC 1446
 QY 1438 GCTGAGCTGGTGTGATGATGATGAAACGAGATCTGACCGCTGTCAGTACACCATCA 1497
 Db 1447 GAGAGATGGGAGACATGTCGACATGGTGTGCGCTGACCGAAC 1506
 QY 1498 GCGCTCAAAATGCACTCTGTTGAGCTTATTTGACACAGAGCTGTTCT 1557
 Db 1507 GCTCGAGTGGAGCTCTGTTGGGCTGATGTCACCCGATGCTTAC 1566
 QY 1558 ATAAACCTGAAACACTACGCGAGGCCGACATGCGCAGCTGAGT 1606
 Db 1567 GACCTGGGAAACGAGTCGACTTGGGCTGCTGGCGTATGG 1615
 RESULT 4
 US-09-172-971-7
 ; Sequence No. 7, Application US/09472971
 ; PATENT NO. 6197547
 ; GENERAL INFORMATION:
 ; APPLICANT: SOGO, Kazuo
 ; APPLICANT: YANAGI, Hideki
 ; TITLE OF INVENTION: TRIGGER FACTOR EXPRESSION PLASMIDS
 ; FILE REFERENCE: 1422499P
 ; CURRENT APPLICATION NUMBER: US/09/472,971
 ; CURRENT FILING DATE: 1999-11-28
 ; EARLIER APPLICATION NUMBER: WO98/372965
 ; EARLIER FILING DATE: 1998-12-28
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 7
 ; LENGTH: 4524
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli
 ; US-09-472-971-7
 Query Match 36.0%: Score 589.8: DB 4: Length 4524;
 Best Local Similarity 61.3%; Pred No. 5.8e-164; Mismatches 617; Gaps 6; Gaps
 Matches 986; Conservative 0; MisMatches 617; Indels 6; Gaps
 QY 4 GCAAAAGAACTTTCAGCAGATTCGGCTGCTGCGATGTTGATG 63
 Db 389 GCTAAGACGCTAAATTCGGAAACGACCCCTGTCGAATGCTGGCGCGTAACGTA 448
 QY 64 TTAGCGATAACCGTCAAAGTACGCTGTTGCTCTAAAGGCCGAATGTTGTCGTGAA 123
 Db 449 CTGGAGATCGAGTAAATTCGGAAACGACCCCTGTCGAATGCTGGCGCGTAACGTA 508
 QY 124 GCTTGTGTTCTTAAATTAATGACGGGTAACTATGCTAAAGATGTTAAGAGTGGATA 183
 Db 509 TCTTTGGTGTGCAACGACATACCAAAAGATGTTGCTGGTGTGCGTAACTGGACTG 568
 QY 184 GAGACATTTGAAACATGGGACAAATGGGCTGAGTGGCTCTAAACCAT 243
 Db 569 GAGACAAAGTGTGAAATATGGGCGAGATGGAGAAGAAGTGGCTCTAAAGAAC 628
 QY 244 GATATGCTGTTGATGCGACGACTACGTCACAGCTTGGACACGCTTCTGAA 303
 Db 629 GAGCTGATTTGAACTGGGACAAATGGGCTGAGTGGCTCTAAACCAT 688
 QY 304 GGTCTAAATGACGAGGGGCTGCTGAGGTTATCCCGCGCGCATGAA 363
 Db 689 GGTCTAAATGACGAGGGGCTGCTGAGGTTATCCCGCGCGCATGAA 788
 QY 364 GCAACGACACGCTGTTGAGCTGAAACCTATGCTCAACCTGTTGTCGCAAGGA 423
 Db 749 GGCTGTCAGCGCGACGCTGAGGACTGAAAGCTGTTGCTGTCGTTGCTGACTCAA 808
 QY 424 GCTATGTCAGCTGCGAGTATCATCACGCTC--TGAAGATGTTGAGATATC 480
 Db 809 GGATGTCAGCTGAGGTTGACATCTCCGCTAATCCGCGACAAACCTGTTGAGCTG 668
 QY 481 TCAAGACCTATGGGGGGGGGAGGAGTGGTGTGTTACCATGAGAATCTGAGGT 540
 Db 859 GCTGAGCTGATGGCAGACATGGCTGAAAGAAGCCGTTACCGTGGAGCGTACCGT 928
 QY 541 ATGAAACAGACTGAGTGTGGAGCATCAATTGCCCTGGTTACCGTGGAGCTCAA 1006

1800 *Neurotoxigenic C. difficile* ATCC 25070 1749
 QY 181 *TAGAGAGATCATTTTAAACATGGGACAAATGGTGTGAGTGTGCTGACTGAC* 240
 Db 1748 *TGGAGTGCCTTCGCGACACATGGGCCAGTGGTGAAGAAGTACCC* 1689
 QY 241 *ATGATATGCTGTTGATGGAGACTGACTGCAACACTTGTACGCAAGCTTAA* 300
 Db 1688 *ATATGCGGAGCGGGTACGCTGAGCTTGTGAACTGCTTCGCGCAGCTTCG* 1629
 QY 301 *GAAGGACTTAAATGTACAGAGGGGCTATGCAATGTTGTTATCGTGAGCTTCA* 360
 Db 1628 *GGGGCTGCAAGACAGCTTGGCAGCAGGCCAATCTCGATGATGTTGAA* 1569
 QY 361 *ACGACAGCGACAGCTGTGAGCTGAGCTTGTGAAACCCATGTCACCTGTTGAA* 1569
 Db 1568 *AAGCTGTAAGCTGTGAGCTGAGCTGAGCTTGTGAACTGCTTCGCGCAGCTTCG* 1509
 QY 421 *GRAGCTATGCTCAGCTGCTGAGTACATCAGCTACGCTC-----TGA* 474
 Db 1508 *TTCGAGATGAGAGCTGAGCTGAGCTGAGCAAGTCCTGCCACAGGAGAGAA* 1449
 QY 475 *TATCTCTAGAGCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT* 534
 Db 1448 *CTCTATGCGGAGCCATGGCAAGGTCAGAAGAAAGGGCTACCGTAA* 1389
 QY 535 *CGAGSTATGAGACAGACTGTGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCT* 594
 Db 1388 *AGGGAACCCGACACTACGCTAGACTGAGCTGAGCTGAGCTGAGCTGAGCT* 1329
 QY 595 *TCTCAATACATGGTACAGACAGCTGAAATGGTCCAGACCTTGAAACCCATTTC* 654
 Db 1328 *TCTCCCTACTCTGTAACGACAGGGTAGATGGAGCTGCAATGAAACCTTC* 1269
 QY 655 *TTAATCAGGTTAAAGTGTCAACATCCAAAGACATTGCTGCACTTGAGAGT* 714
 Db 1268 *CTCTCACGACAAATACTCCSFTCGAAGATGTCCTCGATCTGAAACAG* 1209
 QY 715 *CTTAAACACCGCCATTACTCATATTGCGAGATGTTGGTGAAGACTCCA* 774
 Db 1208 *GTTAGAGGGCAAGCCCTCCATCTGAGACATGCAACGAGACACTGCC* 1149
 QY 775 *ACCTTGGTGTGAGCAAGTGTGTTGTTCACTGTGTTGCTGCAAGGCCAGA* 834
 Db 1148 *ACCTTGGTGTAAACCGTGTGCGCAGCTCAAGTCAGTCAGTGTGCAAG* 1089
 QY 835 *TCTGTGATCTCTGTAAGCTGTGAGAGCATGCTATCTGACAGCTGAGCT* 894
 Db 1088 *TCCGGAGCTCTCGAGGCTATGTCGAGACATTCTCGAGGGGGACGTT* 1029
 QY 895 *ATTACAGAGGGCTGAGCTGATTAAGATGCTACATGAGACCCCTGGACAGT* 954
 Db 1028 *ATCAGCGAGAGACGGCTGAGGTGAGATGCTACGGTGGATATGCTGGTAC* 969
 QY 955 *GCTAGAGTATGAGTAAAGATGACAGCATGTTGAGGTAGTCGAA* 1014
 Db 968 *GAGAACTTACGGTTGATGAGACAACTACTCTGTTACGGCGGAAACAGAA* 909
 QY 1015 *GCTATGCTAACGGTATGCACTGATTAATGCCATTGAAACACACTCTGAC* 1074
 Db 908 *GCGCATCGCTCACGTTACGCAAGTCAGATGGAGATGAGACAGCTAC* 849
 QY 1075 *GACCGTGAACACTCAGAGCTGGGAATTTAGCTGTTGTTGTTAGTTAA* 1134
 Db 848 *GACCGCGAAAGCTCGCAAGACGTTGGCAAGCTGCGCGGGTGTAGCTT* 789
 QY 1135 *GTAGGAGCTCCAAAGACAGCTTAAAGAACTTGCGATGAGGAGCTA* 1194
 Db 788 *GTGGGTGCTGCCAGGAGTGGAAAGATGCGTGTAGAGTGCCTG* 729
 QY 1195 *ATGGCTCACCTGAGCGGTGAAAGTATGCTGTTGTTGTTGAAACAGCTT* 1254
 Db 728 *AGTCGAAAGCGCTGCTGCACTGAGGGTACAGTGTACCGGGTGTAGCTT* 669
 QY 1255 *ACGTTGAAAGTGGAGCTCTGCTGAGTGGGAGTGTGACTGAC* 1314
 Db 668 *CGTCCTAAGTCGCTTGTGAAAGTGTGCAAGGGTGAAGAGACAAACAGGAT* 609
 QY 1315 *--ATTGCTCTGCTGAGAGCTGACGCTAACATGTTAATGTTGTC* 1771
 Db 608 *GAGTCGAAACGGCCATGGAGGAGCGCTGCACTGACGCGTAA* 549
 QY 1372 *GAAGCTCCCTAGTATGAGCTGAAACAGCCGCGAGACAGATTAATGCT* 1431
 Db 548 *GGGGTCCGGTGTGTTGAGCTGAGGTGAAGAGGCAAGGAGACTCTGCC* 489
 QY 1492 *CGATCAGGCTCAATGAGCTGACTCTGAGTACCTACCGGTGTTATGACCCGCCCCAGRACA* 429
 Db 428 *CGTGTACATTTGGAAGTACCTCTGCCACCGGCCATGCCGGAGGTATGG* 314
 QY 1552 *GTGCTATAACCTGAAACGCTACGCCAGCCAGTATGCCACGAGTTGG* 1606
 Db 488 *CGTACGATGTTGCAAACCTCTACACTACCGGTGTTATGACCCGCCCCAGRACA* 429
 Db 368 *ATCGCTACAGAAAGAGATAATCTGCCACCGGCCATGCCGGAGGTATGG* 314
RESULT 6
 US 08 470-260-7
 Sequence 7, Application US/08470260
 Patent No. 607706
 GENERAL INFORMATION:
 APPLICANT: Coraci, Antonello
 APPLICANT: Coraci, Antonello
 APPLICANT: Macchini, Giovanni
 APPLICANT: Teiford, John
 APPLICANT: Bugnoi, Massimo
 APPLICANT: Rapuoli, Rino
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: California
 COUNTRY: USA
 ZIP: 94608-2915
 CORRESPONDENCE ADDRESS:
 MEDIUM: COMPUTER
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-POS/MS-POS
 SOFTWARE: Parent release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470/260
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/256,848
 FILING DATE: 21-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: McCullough, Barbara G.
 REGISTRATION NUMBER: 33,713
 REFERENCE/DOCKET NUMBER: 0316.001
 TELEPHONE: (510) 651-2708
 TELEFAX: (510) 655-3342
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1838 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08 470-260-7

Db 58 ATGGCAAAGAAATCAATTTCAGATAGTGGCGGAAACCTTTTGAAGGGGAG 117
 Qy 61 ATGTTAGCAGATACCGTCAAGTAACTGCTTAAAGGGGAAATGTTGTC 120
 Db 118 CAACTCAGACGACCTGTCAGAAAGTACCATGGGGCAAGGCGAGGATGTTGAA 177
 Qy 121 AAAGGTTTGGCTCCCTTAATCTAATGACGGGGPACCATGCTTAAGAGATGAA 180
 Db 178 AAAGATGATGGCTCAACGATCACACAGGGCAAGGCGAGGATGTTGAA 237
 Qy 181 TTAGAGATCATTTAAACAGGGACAAATGGTGTGAGGAGTGTGAA 240
 Db 238 TTTAGTTGGCCGTTACTTACAGGGCTTACCTGTAAGAGATGCGAAC 297
 Qy 241 ATGATGATGCTGCTGAGACTCAGACTCAGCTTGTACAGCAACCCATTGAT 300
 Db 298 GCTGTAGTCGCGGGCATGCGAGACGACGACGCCGCTPACITATGCTTTTAA 357
 Qy 301 GAGGACTAAAAATGTACAGGAGGGTGTAACTCAATTGGTATGCTGTTGAA 360
 Db 358 GAGGTTGGAGGATACAGGGTGTGAGCTTGTACCCATTGAGGAGGAT 417
 Qy 361 ACAGAACAGCAGCAGCTGAGCTTGTACCCATTGAGGAGGAT 420
 Db 418 AAAGCTGCTGAGACGCACTTAATGACCTTAAAGGACAAAGTAGGCGTAA 477
 Qy 421 GAAAGTATTGCTGCTGAGCTGAGCTTGTACCCATTGAGGAGGAT 477
 Db 478 GAAAGATCACCAGGGACGATTCGTCAMACTCGATCACAAATGGAAAC 537
 Qy 478 ATCTCAGAGCAGTGGGGCAAGGATGTTGAGCTGTTGATGAA 537
 Db 538 ATCGTGCAGCTGAGATGTTGAGCTGAGGCTGACCGTGGAGCTAG 597
 Qy 538 GGTATGGAAACGAACGACTTGTAGGTTGAGCTGAGGCTGACCGTGGAGCTAG 597
 Db 598 GCGATTGAGATGTTGAGCTGAGGCTGAGGCTGACCGTGGAGCTAG 657
 Qy 598 CAATACATGTCACACAGCATGAAATGGTCAGACCTGAAACCAATTCTCA 657
 Db 658 CCTATTGTTGACGACCTGAGAAATGGCTCAATTGGATAATGCTTACCC 717
 Qy 658 ATCAGGATAAAAGTGTCAACACATCCAGACATTGCAACTCTGAGGATCT 717
 Db 718 TTACGGGATAAAATCTACATGAGACTTCCCGCTACTAGAAACATG 777
 Qy 718 AAAACCAACGCCCTTACATTACTATGAGATGGTGTGAGCACTCCACC 777
 Db 778 AAAGGGGCAACCCGTTTACATGAGACTTCCCGCTACTAGAAACATG 837
 Qy 778 CTGTTCTGAAAGAATGCTGTTGAGCTTCAATGCTGTTGCAAGGCCAGGTT 837
 Db 838 CTATGGTAAATTAATGAGGGTGTGAAATCCAGGGTTAGCTCAGCTT 897
 Qy 838 GGTGATCTGAAAGTGTGAGCTGTTGAGCTGTTGAGGGGAGCTGTT 897
 Db 898 GGGGACAGAAGAAGAAGAATGTCAGACATGCTTAACTGGGGTCAACT 957
 Qy 898 ACAGAGGATCTGAGCTGAAATGAGTGTCAATGCACTGGCTGAGCT 957
 Db 958 AGCGAGGATGTTGCTGAGTAAAGCTGAGTGGATTGAGCTGAGCTGAA 1017
 Qy 958 AGTTACAGTGTAAATGAGCTGACGATTTGCTGAGCTGAGCT 1017
 Db 1018 AGGATGCTGAGTGTCAAGACGACACACAGCATGCTAGATGCAAGGGCATAGCT 1077
 Qy 1018 ATGCTAACCGTATGCTGAAATGCAATTGAGCTGAGCTGAGCT 1077
 Db 1078 GTTAAAGACAGATGCGCAGACGATCAAACCAATTGCAAGGAGGATTGAC 1137
 Qy 1078 CGTCAAACACTCAGAAGCTTGGGAATATGCTGTTGAGCTGTGTTGAA 1137
 Db 1138 AGAAAAATGCAAGAAGATGCTTAACCTCTGCGGGTGTGCTGTTGAAAGTG 1197
 Qy 1138 GGCGCCACAGAGACGACGCTTAAAGAATGAACTTCCATGAGGAGCTTAAT 1197
 Db 1138 GCGCTGCCAGTGGAAATGAGAAGAGAAAGACCCGGTGTGAGCGCTGAGC 1257
 Qy 1198 GGTACAGTGGACCCCTGAGAGGTTGCTGCTGTTGAGACGACTTNTAG 1257
 Db 1288 GCGACTTAAGCGCGGTGAGAGGAGGCGATGTTGGTGGCTGCGCTCATGGC 1317
 Qy 1259 GTTACTGAAAGTAGGCTGAGGAGGTTGCTGCTGTTGAGGAGTGTGAGCT 1317
 Db 1318 GCGCCACAAAGT---GCATTGATTCAGATGAAAGTAGGGTGTGAA 1374
 Qy 1318 GNGCTTCSGCTCTAGAAGAGCTGTCACCPCTTAATGCGGGTACAGGC 1377
 Db 1375 ATCATGCGCCATTAAAGGCCATTAGCTCAATCGCTTCAACAGCTGTTATGATGC 1434
 Qy 1378 TCCGTTGTTATGAGCTGAGTGGAAACAGGCCGCGAGAACAGATTAATGCGCA 1437
 Db 1435 GGTGCGGCGTGTGAGACTGAAACAGGATTTGCTGAGGAGCTTGTGAGGTT 1494
 Qy 1438 GGTGAGTGGGTGATGTTAAACAGGATATTGACCCCTGTCAAAGTACAGCTA 1497
 Db 1495 GCGCAATGATGCGATTTGAAAGGACGATTTGACCCCTTAAGTAGGAAAGGTC 1554
 Qy 1498 GGCCTTCAAGGACCTCTGAGCTGATCTGTTGACGAGAGGATTTGCTGTT 1557
 Db 1555 GCTCTAACAAATGCGTTGCGGTTAACGCTCTTTAACACAGAGACCCGGT---G 1611
 Qy 1558 AATAACACTGACCCAGCTGCGCAGCAGATCCACAGGCTTAAGTAGGAA 1617
 Db 1612 CATGAAATCAGAAGAAAGGAGTCCGCACTGCTATAGTGGGATGGCGGT 1671
 Qy 1618 ATGGCTGGATGGGG 1634
 Db 1672 ATGGGCCATGGGG 1688

RESULT 8
 US-08-166-662-7
 Sequence 7, Application US/08466662B
 Patent No. 6130059
 GENERAL INFORMATION:
 APPLICANT: Coacci, Antonello
 APPLICANT: Bugnoli, Massimo
 APPLICANT: Telford, John
 APPLICANT: Macchia, Giovanni
 APPLICANT: Rappooli, Rino
 TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
 FILE REFERENCE: CIR0057
 CURRENT APPLICATION NUMBER: US/08/466,662B
 CURRENT FILING DATE: 1995-06-06
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 1838
 TYPE: DNA
 ORGANISM: Helicobacter pylori
 US 08 466 662-7

Query Match 32.2%; Score 528.2; DB 3; Length 1838;
 Best Local Similarity 58.9%; Pred No. 5.4e-146;
 Matches 965; Conservative 0; Mismatches 663; Indels 9; Gaps 3;

Qy 1 ATGGCAAAGAAATCAATTTCAGATAGTGGCGGCTGAGCT 60
 Db 58 ATGGCAAAGAAATCAATTTCAGATAGTGGCGGCTGAGCT 117
 Qy 61 ATGTTAGCAGATACCGTCAAGTAACTGCTGCTTAAGGGCAATGTTGCTGAGCT 120
 Db 118 CAACCTCAGATGCTGAGCTGAGGAGGCTGAGGAGGATGTTGAGCTGAGCT 177

QY 121 AACGTTTGTCTCCCTAATACATACAGGGGAAACATGCTAAAGAGCGA 180
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 178 AAAGCTATGCGCTCAGACATCCAAAGACGGCTGCGCTAACAGCTAAG 237
 QY 181 TTAGAGATCATTTGAAACATGGGAAATTGGCTGAAGTGTCTAAACC 240
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 238 TPAAGTGCCTAACTAGCTAACATGGCTAAAGATAGCTAAAGATG 297
 QY 241 AATGATATATGCTGGTATGGAGACTACTGACACAGTTTGACCAAGC 300
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 298 GCTGATGCTGCCGGCATGGCACACGCGACGCGCTAACGGCTAAC 357
 QY 301 GAGGACTAAAKAATATGAGAGGAGGAGGAGGAGGAGGAGGAGG 360
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 358 GAACTTGGAGATATCAGGGTGGGCTAACCTTTGAGCTTAAAG 417
 QY 361 ACAGGAAACGCAACGGCTGTGAGCCTTAAACCCATGCTCACCGT 420
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 418 AAAGCTGCTGAAGGGCTAAATGAGCTAAAGAGGCAAAAGTGG 477
 QY 421 GAGGTTATGCTCAGATGCTGGAGTCACTGGCTGGAGCTGGATC 477
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 478 GAGAGAACTCCTCACTGGCGACATTCGCAACTCCATACATGG 537
 QY 478 ATCTCAGAGCCTATGGGGGGGACAGGCTGTTGATCCTGAGCTG 537
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 538 ATCGCTGAGCCTATGCTAAAGGGTGTAGGCTGACCGCTGGAG 597
 QY 538 GCTATGGAAACGACTTGGTGAAGGCTCAATTGACCTGGTTACCT 597
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 598 CAAATACATGGTCAAGAGCATGAAATGGTGCAGACCTGAAACCC 657
 QY 598 GCGCATGGAGGAGTAAATGGTGGCTGGAGGTTGCAATTGCTC 657
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 658 CCTTTATTTGTAACGACCTGAAAGTGGCGCTCAATTGCTTAAT 717
 QY 658 ATCCGGATAAAGTGCACACATCCAGACATTGCGACTACTTGAGG 717
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 718 TTAAGGGTAAACAAATCTGCTGAGTAAAGACATTCGCCGTACTA 777
 QY 718 AAACCCAACGCCATTACTCATTTGAGGAGTGTGATGTTGAGG 777
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 778 AAAGGGGCAACCCGTTAACATCAGCTGAGCTTACGACT 837
 QY 778 CTGCTCTGAGAACATCTGCTGTTCTTCAGTGTGCTGCTCAAGG 837
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 838 CTACTGGTGAATTAAAGGGCTGTGATTCACCGGGTAAAGCTC 897
 QY 838 GGTGATCTGTAAGCTATGCTGAGCATGCTATCTGAGCTGATG 897
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 898 GGGGACAGAAGAAGAAGAATGCTCAAGACATGGCTATTACCG 957
 QY 898 ACAGAGTCCTGGACTGTAATTAAAGGTCTACATGACGCCCTGGAC 957
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 958 AGCCAAAGATGGCTTGGCTAGAAACGGCTGAGTGGAGGTTAG 1017
 QY 958 AGATTCAGTGTAAAGATGACAGTAATGTTGGAAAGTGTCAAGA 1017
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1018 AGGATGTTGATGCTGAAAGACACACCGATGCTGAGTGGAGG 1077
 QY 1018 ATGGCTTACCTTGTGACTGATTAACGCAATTGAAACACAC 1077
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1078 GTTAAAGACAGCTGGCTGCGCAGTCAAACCAATTGCTGAG 1137
 QY 1078 CGTCAAACATCAAGAAGCTTGGGAAATTAGTGGGGCTACTCT 1137
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1138 AAGGAAATGCTGAGAAGATGGCTAACTCTGGGGTGTGCTG 1197
 QY 1138 GAGCTTCAACAGAGACGCTTAAGAAGAACTCTGGCTAACTCT 1197
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1198 GGCTGCTGAGTGAATGAAAGAGAAGACCGGGTGTGACGGCTG 1257
 QY 1198 GCTACAGTGTGCGCCGTTGAGAAGGTATGCTGCTGGTGAAG 1257
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1258 GCGACTTAAGGGGGCTGAGAGGCTGTTGCTGCTGGGGCTCATG 1317
 QY 1258 GTTATTGAAAGTGTGAGCTGCTTGTGCTGAGGAGATGCTACTG 1317
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1318 GCGCTCAAAAGT---GCAATTGTTGAGTGTGAGTAAAGTGG 1314
 QY 1318 GTGCTTGTGCTTGTGAGGCTGACCTCAATGCTTAATGCTGGTCAAG 1337
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1375 ATCGGCGCCTAAGGCCATAGCTCAATGCTACAGCTGCTGTTATG 1434
 QY 1378 TCCCTACTTATGCAAGCTGAAACCCATGCTCACCGTATCTGCG 1437
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1435 GGTGIGICGIGTGAAGGAAACGGGCTTGTGTTAACGCTGAAAT 1434
 QY 1438 GGTGAGGGGGTGTATGATTAACAGGAATCATTGACCTGCTCAAG 1497
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1495 GGCAGATGTGGTATGTTTAAAGAGGCTTATGACCCCTAAAGTGA 1554
 QY 1498 GCGCTTAAATGAGCTCTGAGCTGCTTATTTGACACAGAAGGTTAATGCTG 1557
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1555 GCTCTACAAATGGGTTCTGGTTCAAGCCGCTTTRCCACRAGGC 1611
 QY 1558 ATAACAGCTAACCGCTACGCCAGGCCAGCAGGCTGATCCAGGAT 1617
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1612 CATTAAATCAAGAGAAAGACCTCCGCACGCTGGATGGCTGGGGT 1671
 QY 1618 ATGGGGGGTGGGG 1634
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 1672 ATGGGAGCATGGGG 1688

RESULT 9
 US-08-256-847C-6
 Sequence 6, Application US/08256847C
 Patent No. 6403099
 GENERAL INFORMATION:
 APPLICANT: Rappoli, Rino
 APPLICANT: Cestantino, Paolo
 APPLICANT: No. 0099611, Francesco
 TITLE OF INVENTION: Conjugates Formed From Heat Shock Proteins And Oligo or Polysaccharides
 FILE REFERENCE: CHIN-004-2
 CURRENT APPLICATION NUMBER: US/08/256,847C
 CURRENT FILING DATE: 1994-11-01
 PRIOR APPLICATION NUMBER: PCT/EP93/0516
 PRIOR FILING DATE: 1993-03-08
 PRIOR APPLICATION NUMBER: FI9A000058
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 6
 LENGTH: 1838
 TYPE: DNA
 ORGANISM: *H. pylori*
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (58)-(1695)
 OTHER INFORMATION:
 US-08-256-847C-6

Query Match Score 528.2; DB 4; Length 1038;
 Best Local Similarity 58.9%; Pred. No. 5.4e-16;
 Matches 965; Conservative 0; Mismatches 663; Indels 9; Gaps 3;
 QY 1 ATGGCAAAAGAATCAATTGCTGAGGCGCGCTCTGCATGCGGGAGCTG 60
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 58 ATGGCAAAAGAATCAATTGCTGAGGCGCGCTCTGCATGCGGGAGCTG 60
 QY 61 ATGGTACAGATGGCTCAAGTAAAGCTGGTCTTAAGGGCCAAATGTTGCTGTGA 117
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| 118 CAACTCATGAGCCTGCTCAAGTAACCTGGGCCAGGGCAGGAATGTTGATC 177

QY 121 AAGCTTGTGTCCTTAATCTAATGAGGGTACCATCTTAAGAGATGAA 180
 Db 178 AAGCTTGTGTCCTTAATGAGGGTACCATCTTAAGAGATGAA 237
 QY 181 TTAGACATCTTGTAAACATGGGCAATGAACTGAACTGAACTGAA 240
 Db 238 TTAGTGGCCAGCTAACATGGGCAATGAACTGAACTGAACTGAA 297
 QY 241 ATGATATGTTGGTGTGATGGGACGACTACTGCAACAGTGTGAC 300
 Db 298 GTGATGCTCGCGCGATGGCACGACACGCGCTGACCTGATGAA 357
 QY 301 GAAGCTTAAATGTCACCGAGCTTACCTATGGTTCGGTCAAGGAA 360
 Db 358 GAGGTTGGAGGATATCAGCGTGGCTTAACCTTATGAAAGGAG 417
 QY 361 ACAGCAACAGCAACAGCTGAGCTGAGGCTTGTAAAGSCATGCT 420
 Db 418 AAGCTCTGAGGGATCATTAAGCTTAAAGGAAAGGAGGAGGAA 477
 QY 421 GAAGCTTGTCTCAGGCGTCACTACCTACCCCTGAAAGTGGAGAT 477
 Db 478 GAGAAATCTACCCGAGCGACATTCTGCAACTCGATCACATCGGGAA 537
 QY 478 ATCTCAGAAGCTGATGGGCGTGGCTGGACAGCTGGTGTGATTCGA 537
 Db 538 ATCGCTGACCTTAAAGGAAAGTGGTAAAGCGCGTACCCGGAGGAA 597
 QY 538 GGTATGAAACAGCTGATGGTGTGAGGATGCAATTGACCGTGTAC 597
 Db 598 GCGATGAGTAAATGGTGTGAGGATGCAATTGACCGTGTACCC 657
 QY 598 CTTATTTGTTAAAGGAGCGTACAGATGAAATGGTGGAGCTTAAAC 657
 Db 658 CCTTATTTGTTAAAGGAGCGTACAGATGAAATGGTGGAGCTTAAAC 717
 QY 659 ATCACCGATAAAAGCTAACATCACATGAGCATTTGCGACTACTGAGGAT 717
 Db 718 TAAACACACCGTCATRACTCATPATCGACATGTTGAGGACTTCACC 777
 QY 718 AAACACACCGTCATRACTCATPATCGACATGTTGAGGACTTCACC 777
 Db 778 AAAGGGCAACCGCTTAAATGAGCTAACATCACATGAGCATTTGAGGACTTAAAGGCT 837
 QY 778 CTGTGCTGACAGATCTGGACTCTCATGTTGAGGACTTCACCAACCTG 777
 Db 838 CTAGTGTGATTAATTAAGGAGCTTGTGATTCAGGGTAAAGCTCAGCTT 897
 QY 838 CTGTGCTGATTAATTAAGGAGCTTGTGATTCAGGGTAAAGCTCAGCTT 897
 Db 898 GGGGAG 897
 QY 898 ACAGGAGACTTAAAGATGCTTACAGTGGCTTGGAGGGT 957
 QY 898 ACAGGAGACTTAAAGATGCTTACAGTGGCTTGGAGGGT 957
 Db 959 ACGGAGAATGGCTGAGCTTAAAGGAGCTTAAAGGAGCTTAAAGGAG 1017
 QY 959 ACGGAGAATGGCTGAGCTTAAAGGAGCTTAAAGGAGCTTAAAGGAG 1017
 Db 1018 AGAGATGCTGATGCAACAGACACACCGATCTGAACTGAACTGAA 1017
 QY 1018 ATGCTTACCGTATTGCACTGATTAATGCAATGAACTGAACTGAA 1077
 Db 1078 GTAAAGAGAGTCGCGAGTCAACCCAAATGCAACTGCAACAGCTG 1137
 QY 1078 CGTAAAGAGAGTCGCGAGTCAACCCAAATGCAACTGCAACAGCTG 1137
 Db 1138 AAGAGAAATGCAACAGAGATGCAACTGCAACAGAGATGCAACTG 1197
 QY 1138 CGAGTCCACAGAGACCTTAAAGAATGCAACTGCAACAGAGATGCAACTG 1197
 Db 1198 GCGCTGCGAGTCAACAGAGAAAGAGAGAGAGAGAGAGAGAGAG 1257
 QY 1198 GCTAACGTCGAGCTTGTGAGGAGTGTGTTGAGGAGTGTGTTGAGGAG 1257

RESULT 10
 US-08-467-822-28
 Sequence 28, Application US/0847822
 Patent No. 5843660

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Sauerbaum, Sebastian

APPLICANT: Ferreiro, Richard L.

APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNODIRECT COMPOSITIONS AGAINST
 TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
 TITLE OF INVENTION: COMPOSITIONS AND NUCLEIC ACID SEQUENCES ENCODING SAID
 TITLE OF INVENTION: POLYPEPTIDES
 NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnean, Henderson, Farabow, Garrett &
 STREET: 1300 1 Street, N.W.
 STATE: Washington
 COUNTRY: USA
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467, 822
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435

APPLICATION NUMBER: US 08/447, 177
 FILING DATE: 19-MAY-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/432, 697
 FILING DATE: 02-MAY-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 03495.0137-02000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-0000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 224 base pairs
 STRANDEDNESS: double
 TOPology: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-467-822-28

Query Match 30.3%; Score 496.2; DB 2; Length 2284;
 Best Local Similarity 58.2%; Pred. 0; Mismatches 673; Indels 12; Gaps 4;
 Matches 952; Conservative 0; Mismatches 673; Indels 12; Gaps 4;

Qy 1 ATGGCAAAAGAAATCAATTTCAGCGATGCGCTGCGTGCAGTGCGGGAGTTGAT 60
 Db 506 ATGGCAAAAGAAATCAATTTCAGCGATGCGCTGCGTGCAGTGCGGGAGTTGAT 60
 Qy 61 ATGTTGAGATACCCGTCAGCAAGTACCGCTTGCTTAAAGGCCTAATGGCTCTGTA 120
 Db 566 CACTCCATGAGCTCTCAAGAACCATGGGGCAAGAGCAGGAGCTGTGTCCTA 625
 Qy 121 AAAGCTTGGCTCCCTTAATCTAATCTAATGACGGGTACCATGCTAAAGATCGA 180
 Db 626 AAAACATATGGGCTCAAGCAACCAAGAACGGCTGCGCTGGCTAAAGATGTA 685
 Qy 181 TTAGAGATCATTTGAAACATGGGCAAAATTGGTGTGAGTGTCTCTAAACC 240
 Db 686 TTAACTGGCCCGTGCCTACAGGGCTCACTCTTAAAGAGATGCGAACACC 745
 Qy 241 ATATGATATGCGGTCATGGACGACACTGCAACATTGACAGGATGCTAT 300
 Db 746 GTGTGATGCCGGCATGGCACGACGACCTGGCTTATAGCTTTAA 805
 Qy 301 GAGGACTAAATATGACAGCAGGAGTGTATCCGCGAGGTAA 360
 Db 805 GGGCTTGAGGAAATCACGGCTGGCTAACCTTATGAGTGAACAGGCTG 865
 Qy 361 ACAGGACACGACACGGCTGTGAGCTTAAAGCCATGCTCAGCTGAG 420
 Db 866 AAAGGCCCTGAAAGCATTTATGAGCTTAAAGAGCGCAAAAGTGGGTTAA 925
 Qy 421 GAGCTATGCTAGCTGGCTGGAGTATCACGGCT --TGAAGAATGGAGAT 477
 Db 926 GAGAAATCACCGAATGAGCACTTCTGCAACCTGGATCACAAATGGAACT 985
 Qy 478 ATTCAGAGCTATGGGCTGGCCACAGGCTGATTCACCTGGAGATCTCGA 537
 Db 986 ATCGGTGAGCTGTGAAAGGGTGTAGACGCGCTGACCGTGGAGACTAG 1045
 Qy 538 GGTAGGAAACGAGCTGGTGAAGGGCATGCAATTGACCGCTGGTACTCT 597
 Db 1046 GGCTTGAGATGAAATTAGTGTCTGTAGAGGCTGCAATTGATAGGGCTACCTCCTC 1105
 Qy 598 CAATCATGCTGAGCATGAAATGTCAGACATGAACTTCAGACATTGCA 657
 Db 1106 CCTTACTTGTGAAACGACCTGGAGAAATGACGCCCTAACGGCTTACCTCT 1165
 Qy 658 ATCAGGATAAAAGTGTCAACATCAGACATTGCACTCTGGACTCTGGAGTTCT 717
 Db 1166 TTAACTGATTAATTAATCTCTGCTGAGACATTCCTCCGCTACTAGAAAACCTG 1225
 Qy 718 AAACCAACCGTCAATTCTCATATGAGATGATGTGATGGTGAAGCACTTCACC 777
 Db 1226 AAAGGGGCAACCGCTTAACTCATGCGAGACATTGGCGAGCTTAACGACT 1285
 Qy 778 CTGCTCTGAAAGATGCTGTTCTCACTGGTGTGCAAGGCCAGATT 837
 Db 1286 CTAGTGTGAAATTAAGGGCGTGTGAAATTCGCGGTTAAGCTCAGCTT 1345

Qy 838 GGTGATGCTGTAAGCTCATGCTGTGAGCATGCTCTGAGCTGTTACGGTATT 97
 Db 1346 GGGACAGAGAAAGATGCTCAGCATGCTGTTTAACCGGGGCGTCAAGTCATT 1405
 Qy 898 ACAGAGATCAGACTGTAATTAAGATGCTACATGTCACCCUTGCAAGGGCT 957
 Db 1406 AGGRRASATGGCTGAGCTGTTAAGCTGAGCTGAGCTGAGCTGAGCTG 1462
 Qy 958 AAGTTTCACTGAGCTGAGCTGTTAAGCTGAGCTGAGCTGAGCTGAGCT 1017
 Db 1463 AAGTTTGTGATGCAAGACACACCGATGCTGAGATGCAAGGCCATAGCCATG 1522
 Qy 1018 ATGCTTACCCATGCTGATGCTGTTAATGCTCATGAGAACACAACCTTGACTG 1077
 Db 1523 GTCAAAACAGAGCGCCAAATCACAACCAATATGCGACGACAGGAAAGTAGAC 1582
 Qy 1078 CGTCAAAACCTCAGACAGCTTGGCAAAATTAGCTGGTGTAGCTTCAAGTA 1137
 Db 1583 AAAGAAATATTGCGAAAGATGGCCAACACTCTGGCGGTGCGCTGTTAAGTG 1642
 Qy 1138 GGACTCTCAGAGACGCGCTTAAAGGAATGAAACTCGATTTGGGGTGGCTTAAT 1197
 Db 1643 GGCGCTCGAGCTGAGTGAATGAGAAATGAGGAAAGACGGGGTGGATGACGGTTAGC 1702
 Qy 1198 GCTCACTGCTAGCGTGTGAGAATGAGCTGTTGTTGTTGGAACACTATAGC 1257
 Db 1703 GGACTTAACGGGGTGTGAGAGCTGTTGTTGTTGGGGCTGGCCCTCATGCC 1762
 Qy 1258 GTTATTGAAAGTGTGCTCTGAGCTGTTGAGGGGAGTGTCTACTSGACGTTACATT 1317
 Db 1763 GCGCCCAAAGT--GCATTTGATTTACGATGATGAAAATGGCTATGAATC 1819
 Qy 1318 GTGCTTGTCTAGAGAGGCTGTACGCTCAATGCTTAATGCTGGTAGGAGGC 1377
 Db 1820 ATCGTGGCCATTAAGCCCATTTGCTCAATGCCGTTATGAGGG 1879
 Qy 1378 TCGTACTTATGACAACTGAAACAGGCCCTGAGGAACAGGATTATGGTGCACA 1437
 Db 1880 GGTGTTGCTGTAATGAGTGAACAGGAGGGATTGTTACGCTAGCAAT 1939
 Qy 1438 GTGAGCTGGGTGATGTTAAACAGGAACTGACCTGCTCAAACTACATCA 1497
 Db 1940 GCGAAGTGTGGACATTTTAAAGAGCATTTGACCCCTTAAGATGAGGATC 1999
 Qy 1498 GCGCTTAAATGGAGCTCTGAGCTGTTGAGCTTATTTGACACAGAGCTGTTGCT 157
 Db 2000 GCTTACAAATGGTTCTGTTCAAGCCCTGCTTAAACACAGACCGT--G 2056
 Qy 1558 ATTAACCTGACCGCTCCACGCCGGCAAGATGCCCGAGGTATGGTCAAGGAT 1617
 Db 2057 CATTAAATCAAGAGAAAGCGGCCCAACATGCTTATGGGGCATGGGG 2116
 Qy 1618 ATGGCTGGATGGCGG 1634
 Db 2117 ATGGAGGCGTGGGG 2133

RESULT 11
 US-08-432-697-28
 Sequence 28 Application US/08432697
 Patent No. 6248330

GENERAL INFORMATION:
 APPLICANT: Labigne, Agnes
 APPLICANT: Sauerbaum, Sébastien
 APPLICANT: Ferrero, Richard L.
 APPLICANT: Thibierge, Jean-Michel
 TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
 HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
 COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
 TITLE OF INVENTION: POLYPEPTIDES
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESSE:

ADDRESSEE: Flanagan, Henderson, Farabow, Garrett & Company, Dunbar Street, 1300 I Street, N.W., Washington, D.C., USA, ZIP: 20005-3115

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US08/432,697
 FILING DATE: 02-MAY-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Mehl, Kenneth J.
 REFERENCE/DOCKET NUMBER: 23-146
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-0000
 FAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2284 base pairs
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic) US-08-432-697-28

Query Match 30.3% Score 496.2; DB 4; Length 2284; Best Local Similarity 58.2%; Pred. No. 1.7e-136; DB 673; Indels 12; Gaps 4; Matches 952; Conservative 0; Mismatches 673; Indels 12; Gaps 4;

QY 1 ATGGCAGAAAGAACTCAATTTCAGCAGATCGCGCTGTCGATGGCCGAGATG 60
 QY 506 ATGGCAGAAAGAACTCAATTTCAGATGCGAGAAACCTTTATGAGGGTAAAGA 565
 QY 61 ATGGTACGAGATGCCGCAAGATACGCTTGGCTTAAGGGCGGATTTGCTGAA 120
 QY 566 CAACTCCAGAACGCTGTCGAAGTACCGTCAAGTACCGGGCAAGGGAGAC 625
 QY 121 AAAGCTTGGTCTCCATTAACTATACGCGGTRACCATGCTTAAGAGATCGAA 180
 QY 626 AAAGCTTGGGCTCAACGATCACCAAGACCGCCAGGGTGTGCTGATGAA 685
 QY 181 TTAGAAGATCATTTGAAACATGGGCAAATTGGTCTGAGTGTCTTAACC 240
 Db 696 TTAATGTCGCCCTGTGCTAACATGGGGCTCAGTCGCTGAAGAGATCGGCAAAAC 745
 QY 241 ATATGATATGCCGCTGATGGAGACTACTGCAAGCTTGTGACGAACTGGCTA 300
 QY 746 GCTGATGGCCGCGCATGCAACGACCCGCGCTGCGCTATAGCAATTAA 805
 QY 301 GAGGACTAAATGTCAGCAGGGCTTAACTTGTATGGTATCGAGGGATGAA 360
 Db 806 GAGGGCTTGGAGAATACCGGCTGGGCTAACCTTGTGAGTGAACGGGATGGAT 865
 QY 361 ACAGCAACGACGACAGCTGCAACGGCCATGCTGAGCTTGAACCCATGTGCA 420
 Db 866 AAAGGGCTCTGAGGATCAATTAGCTGAGCTTAAAGGGGCAAAACTGGCGCTAA 925
 QY 421 GAGGCTTGGTCTGCTGCTGAGTACATGAGCTTAACTGGTATGGAGGCTGAA 477
 QY 926 GAGAACTTCCACGCTAGGGACGCTTCTGCAACCTGGCTCACAAATTCGGAA 985
 QY 478 ATCTGAGAAGCTGGGCTGGGAAACATGTGATTAACATGGAAATCTCTGA 537
 Db 986 ATGGCTGAGGCTATGGAAAGCTGGTAAAGACGGCGCTGACCGCTGAGAGCTAG 1045
 QY 538 GGTATGAAACGACACTGAGGGTGTGAGGCTGATGCAATTGACGGTGTGTTACCTGTC 597

Db 1046 GGCTTAAGATGATTAGTCTGCTTAAGGCTGCAATTGATGAGGCTACCTCTCC 1105
 QY 598 CAACTATGTCAGAGCAAGAAGAAATGGTGCAGACCTGCAAAACCAATTATCTA 657
 Db 1106 CCTACTCTGAAACACGCTGAGAAATGACGCCCTGCAATTGATGACCTGCTACCTT 1165
 Db 1226 AAAGGGCAACGCTTAACTCCCTGAGACATGAGGGCTGAGACACTCCAAAC 777
 QY 658 ATGAGGCTGAAAGATGCAACATCCGAGACATTGCTCCTACTCTGGAGAGTCCT 717
 Db 1166 TTACCGTAAKAAKACTCTCTGATGAGAGACATCTCCGCTACTAGAARAAACATG 1225
 QY 718 AAACACACGCTCATACTCATATGCTGAGATGAGGGTGGAGGCTGAGACCTCCAAAC 777
 Db 1286 CTAGTGTGATAATATGAAAGGGCTGTAATGCAACGGCTTAAGCTCAGGCTT 1285
 QY 838 GGAGACTGCTGAGAATGCTGAGACATGCTGAGCTTACAGGTTACAGGTTAGGTT 897
 Db 1346 GGGGAGGGAGAAGAAGAATGCTGAAAGACATCGCTGTTTAACCGGGCTGCAAGCATT 837
 QY 898 ACAGAGATCTGACTGTGATTAAGAGTCTACATGACGACCCCTTGGAGCAGGTGCT 957
 Db 1406 AGGGAGAAATTGGCTGTGACTGAAACCTGAGTGGAGGAGTGTGAAAGCG 1462
 QY 958 AGATTAAGCTTAAAGATGAGCACAGTAACTGGTGAAGGGTCAAGGAGCTCAGAGCT 1017
 Db 1463 AGATGTGATGAACTACGAGACACGACGATGCTGAGTGGCAAGGCCATTGAC 1522
 QY 1018 ATGGTACCGTTGCACTGATTAATGCAATTGAAACAACTCTGACTCTGACTTGTG 1077
 Db 1523 GTCAGAAGAGTCGGCAATCAAAACCAATTGCAAGCACACGAGCTTCGAC 1582
 QY 1078 CGTGAAGAAACTACAGAACGACCTTGGCAAAATTAGCTGTTGGTGTGAGCTTACAGA 1137
 Db 1583 AAAGAAATATGCAAGAACGATGCGCAACTCTGCGGGTGTGTTAAGG 1642
 QY 1138 GGACCTCACAGAGAGCCTTAAAGAAATGAACTTCGATGAGGCTTAAT 1197
 Db 1643 GGGCGCGCAGTGTGAACTGGAAATGAGAGAAAAGACCGGGTGTGAGCGCTGAG 1702
 QY 1198 GTCACGCTGAGCTGTGAGGAGGTTGTGCTGTTGTGTTGGACGACGACTTATTG 1257
 Db 1703 GGACATAAGCGGGCTGTGAGGAGGTTGTGTTGGTGTGAGCGCTTATTG 1762
 QY 1258 GTTATGAAAGTAGGACCTCTGAGCTGGGGCTGATGCTACTGGAGGTAACATT 1317
 Db 1763 GGGCCCANAACTTGCATGTTGAAATTACCGATGAGAAGATGGGTATGAACTC 1819
 QY 1318 GTCGCTGCTGCTGCTAACAGAGCTGTGCTGCAAAATTCTTAATGCTGTTAACGC 1377
 Db 1820 ATCATGCGGCCATTAAACCCATTAGCTCAATTGCTCAATGCGGTATGATGCC 1879
 QY 1378 TCCGTTGTTATGACGAGTGTGAAACAGCCCTGCTGAGACAGGTTAATGCTCAAA 1437
 Db 1880 GGTGCTGCTGTTAACTGAGTAAACAGCAAGGGCTTGGTGTGTTAAAGCTGACAT 1939
 QY 1438 GTGAGTGGTGTGATGTTAAACAGGATCAACCTGGTCAAGTACAGGATA 1497
 Db 1940 GGCAGATGTTGAGCATGTTAAAGAGGCTTATGACCCCTTAAAGTGAAGGATC 1999
 QY 1498 GGCCTTAATGCGCTGTGAGTCTGCTTATTGACGAGGAGCTGTTGCT 1557
 Db 2000 GCTTACAAATGCGCTGTGCTAACGCTCTTAAACGACGACCTGCTACAGGACACCTG 2056
 QY 1558 ATAAACCTGAAACGACTGCGCTGCGCACTGCAAGGCTTAAAGTGAAGGATC 1617
 Db 2057 CATGAACTAAGAGAAGAAAGGGGCCACGCTGCTTAAACGACGACCTG 2116
 QY 1618 ATGGTGGGATGGGG 1634

Db 2117 ATGGGAGGCATGGCGG 2133

RESULT 12

US-08-466-448-28

Sequence 28, Application US/08466248

Patent No. 6,58559

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Sauermann, Sébastien

APPLICANT: Ferrero, Richard L.

APPLICANT: Thibierge, Jean Michel

TITLE OF INVENTION: IMMUNODUCIVE COMPOSITIONS AGAINST HELICOBACTER INFECTON, POLYPEPTIDES FOR USE IN THE TREATMENT OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finegan, Henderson, Farabow, Garrett & STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,248

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/447,177

FILING DATE: 19-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/432,697

FILING DATE: 02-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495.0137-02000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4000

INFORMATION FOR SEQ. ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 2284 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLogy: linear

MOLECULE TYPE: DNA (genomic)

US-08-466-248-28

Query Match Score 496.2; DB 4; Length 2284;

Best Local Similarity 30.3%; Score 496.2; DB 4; Length 2284;

Matches 932; Conservative 0; Mismatches 673; Indels 12; Gaps 4;

QY 1 ATGGCAAAGAAATCAATTTCACAGATGGCGCTGCGCATGGCGGAGATGAT 60

Db 506 ATGGCAAAGAAATCAATTTCACAGATGGCGCTGCGCATGGCGGAGATGAT 565

QY 61 ATGTTACAGATACCGTCAAGTAACTGCTGTCCTAAMGGGCATGTGTCCTGAA 120

Db 566 CAACTCCATGAGCAGTCAAGTAACTGCTGTCCTAAMGGGCATGTGTCCTGAA 625

QY 121 ATGGCTTGTGCTCCCTTAATACTATAGCGGGTACCTTCTAAGAGATCGAA 180

QY 626 AAAGCTATGGCGCTCAAGCATCACCAAGACGGCTGAGCTGCTAAGAGATGAA 685

QY 181 TTGAGAACATCATTTGAAACATGGGACAAATTGGCTCTGAACTGGCTTCAAAAC 240

Db 686 TTAGTGTCCCCGGCTAACATGGCGCTCGCTGTAAAGAAGATGGCGACAAAC 745

QY 241 AATGATTTCTCTGGTGTGGACGACTACTGCAACAGTTGACACAGCTGTGCT 300

Db 746 GCGATGCCCGCGGATGGACGACCAAGGGCGCGCTGCGCTATGCTTAA 805

QY 301 GAAGGACTAAATGTCAGCAGCAGCTTCACTTCAATGTTGACACAGCTGTGCT 360

Db 806 GAGGGCTGAGGATATACCGCTGGCTAACCTTATGTAAGTGAACAGGCATGG 865

QY 361 ACACCAACAGCACGCTGTAAGCCTTGAAGCCATGTCGAACCTGTATGGAAG 420

Db 866 AAAGCCTCTGGAGGATCTAATGAGTTAAAGAGGAGAAAAGGGCTGAA 925

QY 421 GAAGCTTGTCTGGCTGGCGCTGAGTACATCACCCTATGTAAGTGAACAGGCATGG 477

Db 926 GAAGAACATCACCAGTGCGACCATTTGCAACTCCGATCACATTCGGAAACTC 985

QY 478 ATCTCAGAACATGGGCGTGGCACATGTGTTGATACATCAGAATCGA 537

Db 986 ATGGCTGACCTTATGAAAGTGGTAAGACGGCTGTCACCGTGTGAA 597

QY 538 GGATGGAAACAGACTTGTGAGTGTGTTGAGCAGCATTGACGCTGTTGCTC 1105

Db 1046 GGCATGGAGATGATGAGATGAGCTGACATTCGCTGTCACCGTGTGAA 597

QY 598 CTTACTCTGGTACAGAAATGAAATGGTGGAGACCTTAAACCCATTATCTA 657

Db 1106 CCCTTACTTTTGTACCAAGCTGAGAAATGACCGCTCATGGTAAACCTTAC 1165

QY 658 ATCACGGATAAAAGCTGACATCCACAGATCCACATTTCCACTACTTGAGGAGTCT 717

Db 1166 TTACGGATAAAACATTCAGTGGAGACATCTCCCTACTGAAACACATG 1225

QY 718 AAACACCAACGGTCAATCATCATGATGTCGGATGATGTCGGGGGAGACATTCCACC 777

Db 1226 AAAGAGGCCAACCGCTTTAATCATGTCGAGACATGAGGGGAAGCTTAAAGCT 1285

QY 778 CTGTCATGACAGATCTGGFACTTCATGTTGCTGCTGTCAGGGCGGATT 837

Db 1286 CTGAGTGTGATAATTAACTAGAGGGTTTGTATCGAGCGGTTAACCTCAGGTT 1345

QY 838 GGTGATGTCGTTAAGCTTATGCTGTGAGCAGTCATCTGTCATGTCAGTGTGTCAGT 877

Db 1346 GGGGAGGAGGAAAGAAGAGCTCAAGATCGCTGCTTTAACCGGGGTGAGCATT 1405

QY 898 ACAGAGGATCTAGACTTGTAAAGATCTAATGAGCTGAGCCCTTGGAGAGGTGCT 957

Db 1406 AGCGGAAATGGCTGTGACTCTGAAACGCTGAGTGGTTTGTAGCA---AGGG 1462

QY 958 ATGATTCAGTGTATAAGTAGGACAGTATGTGAGGTCTGGAGGTCTGGAGCT 1017

Db 1463 AGATGTTGATGACAGACGACGACGACGCTGGATGGCGCTGGCATGGCTG 1522

QY 1018 ATGCTTACCGTATTGCACTAACTGCAATTGAGAACACTCTCTACTTGAC 1077

Db 1523 GTCAAGACAGAGTCGCGCAATCAAACCCAAATGCAAGCAGACAGCAGCATGGAC 1582

QY 1078 CTGAAACATCACAAACCTGGCAATTGACTGTGGTGTGGAGCTTCAAGATA 1137

Db 1583 AAAGAAATGCGAGAAATGGCTGCGGAGTGGCTGCTCTGCGGTTGGTGTGAA 1642

QY 1138 GGGCTCCACAGAGCACTTAAAGAGATGAACTCTCCATGAGATGCTTAAT 1197

Db 1643 GCGGCTGAGTGGAAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1702

QY 1198 GGTACAGTCGACCCGGTGGAGGAGTGGTCTCTGGTGGAGACGACTTAAAG 1257

Db 1703 GCGACTAAAGCGCGGTTAGAGGCGATTGTTGATGCGGCGGCGCCATGCG 1762

QY 1258 GTTATGAAAGTAGCAGCTCTGAGCTGAGGCGATGACTCTGACCTAACTT 1317
 Db 1763 GGGCCCAAAGT--GCATTGTTAATTCAGCTGATGAAAGTGGCTATGAAATC 1819
 QY 1318 GTCCTTGCTCTAGAGAGCGCTGAGCTTAACCTGTTAACTGCTTAAAGGGC 1377
 Db 1820 ATCATGGCCCAATTAGGCCATTAGCTCAATGCTAAATGCTTAACTGCTTAAAGGC 1879
 QY 1378 TCGTAGTTTACAGTGTGAAACACGCCCTGAGCAGGAACTGCTTAAAGGGC 1437
 Db 1880 GTCAGTGTGCTGAGTGTAGAGTGTAGAAACACGCCCTGAGCAGGAACTGCTTAAAGGC 1939
 QY 1438 GTCAGTGTGCTGAGTGTAGAGTGTAGAAACACGCCCTGAGCAGGAACTGCTTAAAGGC 1939
 Db 1940 GCGCAACTATGTCAGCTTAAAGGGCTTAAAGTAAAGTAAAGGATC 1999
 QY 1498 GCGCTCAAATCAGCTCTGAGCTTAAAGGGCTTAAAGTAAAGTAAAGGATC 1999
 Db 2000 GCGTTACAAATGGTTGGTTTCAAGCTGCTTAAACCGAACCTTAAAGTAAAGGATC 2056
 QY 1558 AATAAACCCTGACGACGCTGCCGCGCAATGCCAGCGGGTATGGATCCAGGATG 1617
 Db 2057 CATGAAATCAAGAAGAAAAGCGGCCCAAGCTGTATGGTGGCATGGGGGA 2116
 QY 1618 ATGGGGGGATGCGCG 1634
 Db 2117 ATGGGGGGATGCGCG 2133

RESULT 13

; Sequence 3, Application US/08955565A
 Patent No. 6331398
 GENERAL INFORMATION:
 APPLICANT: Miroslav
 TITLE OF INVENTION: Immuno Response Enhancer Therapy
 FILE REFERENCE: WARE-03625
 CURRENT APPLICATION NUMBER: US/08/955, 565A.
 CURRENT FILING DATE: 1997-10-17
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patentin version 3.0
 LENGTH: 4380
 TYPE: DNA
 ORGANISM: Mycobacterium tuberculosis
 US/08/955-565A-3

Query Match 28.0%; Score 458.6; DB 4; Length 4380;
 Best Local Similarity 55.8%; Pred. No. 3.1e-125;
 Matches 875; Conservative 0; Mismatches 694; Indels 0; Gaps 0;

QY 1 ATGCCAAAGAACATCAATTTCAGCAGAGCGCGCTGCGCATGGGGGATGAT 60
 Db 252 ATGGCCAAAGACATTCGGCTGAGGAGAGCGCGCTGCGCATGGGGGATGAT 311
 QY 61 ATGGTAAAGATGATGCTCAAGTGTGCTTAAAGGCCCAATGTTCTTAA 120
 Db 312 GCGCTCGGATGCGCTTAAGGGCATGGTGGCTGAGGAGCTGCGCATGGGGGATGAT 371
 QY 121 AAAGCTTGGTCTCCCTTAATTACTATGACGGGTAACCATGCTAAAGATGCGA 180
 Db 372 AAAGAGTGGGCCCCACGTCACCAAGATGCTGCTGCTCATGCCAAAGGAGTCGAG 431
 QY 181 TTAGAGATCATTTGAAACATGGGCAAAATTGGTGTGCTGAGTGGCTTAAAC 240
 Db 432 CTGGAGGATCCCTAGAGAGATGCGGCCGACGCTGCTAAAGGGTGGCCAGAGGCC 491
 QY 241 ATGATATGGCTGCTGATGGAGCAGCTACTGCAACAGTTGACACAGCTTGTG 300
 Db 492 ATGGAGCTGCGCTGACGCCACGCCACCTGCGGCCAGGCTTGCGTGGCTG 551
 QY 301 GAAGCACTAAAGATGCTCAAGTGTGCTTAAAGGCCCAATGTTCTGAGGCTTAA 360

Db 552 GAGGCCCTGCCAAGTCGCCGCGCCGCGCCAAACGGCATCGAA 611
 QY 361 ACAGGAACAGCACAGCTGAGCTTGAAGGCTTGAAGCCATTCTGATCAGGGCAG 420
 Db 612 AAGGCGGGAGAAGTCACCCGAGCCCTGCTGAAGGCCCAAGGGCCAGGGAG 671
 QY 421 GAGCTATGCTCAGTCCTCGAGTATCATCGCTCGCTGAAGAAGTGGAGATATC 480
 Db 672 GAGCAGATGGCGCCACCCAGGGTGGCGGTGACCAAGTCATCGGTGACCTGATC 731
 QY 481 TCAGAGTGTGGACCTGGCGACCGTGGCGACGCTGCGCATACATGAGGATTCGAGT 540
 Db 732 GCGGGGGATGACAAAGTGGCGACAGGGCTCATCCCTGGGGTCAACACC 791
 QY 541 ATGGAAACAGACTGAGTGAAGTGGTGGAGGCAATGGCAATTGAGGTTGGTGTGCT 600
 Db 792 TTGGCGCGAGCTGAGCTCACCTGACGGGTATCGGTTCGCAAGGGCTACAGTCGGG 851
 QY 601 TACATGGCACAGAACATGGTGGCGACCTTGAAGAACCTTATCTTAACT 660
 Db 852 TACTCGTGTACCGACCCGGCGTGTGACATGCCGAGGAGGGTGTGACCCCTG 911
 QY 661 ACGATAAAAGCTCAACATCCAAAGACATTTGGCAACTCTGAGGAGTCTAA 720
 Db 912 GTCAGCTCAAGGTTCCACTCTCAGGTTGCTGAGGTTGCTGAGGATTCGGGA 971
 QY 721 ACCACCTCCATTACTATTTTCAGATGATGTTGAGCTGAGCTCCACCTTCACCCCT 780
 Db 972 GCGGGTAGCGCTGTGCTGACATGCCGAGGAGGGCGCTGACCCCTG 1031
 QY 781 GTCCTGACAGATGCTGCTGACTTCAATGCTGAGGTTGCTGAGGATTCGGGA 840
 Db 1032 GTCCTCAACAGATCGGGCACCTCAGTCGGTGGCTCAGGGTCTCCGGCTTGGC 1091
 QY 841 GATGGTGGTAAGCTATGTTGAGACATTTGGTGTATCTTGTGAGCTGAGGATTCAC 900
 Db 1092 GACGGCGCAAGGGGAGCTGCGAGGATGCGCATCTCACCGGGTGGAGGATCAGC 1151
 QY 901 GAGGATTTAGACTGTTAAAGATGCTCAATGAGCACCCCTGGGGGATGCTAAG 960
 Db 1152 GAAGGGCGCCTGACCCCTGAGGAGCTGCGGAGGAGTCAGGCCCGACAG 1211
 QY 961 ATTACAGTTGATAAGAGGAGCAGCTGAGTGTGAGGTTGGAGGTTGAGCTT 1020
 Db 1212 GTCCTGTCACCAAGGGAGACCCATGCTGGGGGGTGTACACGGCCATC 1271
 QY 1021 GCTACCGTATGCTGACTTAACTGCAATGAAAGACACACTCTGACTTGTGCGT 1080
 Db 1272 GCGGGAGGCGGCCAGATCGCGCAGGAGTCGAGCTGAGGAGTCGAGACGGACCCGACGG 1331
 QY 1081 GAAAGACTACAGAACGCTTGTGCAATTAAAGGAATTATGGTGGGGTGGCTTAAAGTGG 1440
 Db 1332 GAGAGTTGGAGGAGGCGCTGAGCTGCGCTGAGGAGTCGAGACGGACCCGACGG 1391
 QY 1141 GCTCCAAACAGAACGAGCTTAAAGGAATTGAAACTCTGCGATTGAGGATCTCTAAATGCT 1200
 Db 1392 GCGCCACCGAGGCGACTCAAGGGGCCAGACCGCATGGAGATGCGCTTCAAT 1451
 QY 1201 ACAGGCGACCCGCTGAGGAGGATGCTGCTGAGGAGACGACTTATGCGT 1260
 Db 1452 GCGAGGCCGCGCTGAGGAGGCGCTGAGCTGCGCTGAGGAGTCGAGGCG 1511
 QY 1261 ATGGAAACAGTACAGGAGCTGAGCTTAAAGGAATTGGTGTGAGGATCTCTAAATGCT 1320
 Db 1512 GCGCCACCGAGGCGACTCAAGGGGCCAGACCGCATGGAGATGCGCTTCAAT 1571
 QY 1321 CTGGCTGCTGAGAGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGGCTC 1380
 Db 1572 ATGGTGGCTGAGGAGGCCGCTGAGGAGTCGCTGCTCAACTCGGCTGGGGCC 1631
 QY 1381 GTAGTATGACAGTGAAGAACAGGCCCTGAGGAGGTTAACTGCTCCACAGT 1440

RESULT 15
 US-09-103-840A-1
 Sequence 1, Application US/09103840A
 Patent No. 629438
 GENERAL INFORMATION:
 APPLICANT: FLEISCHMAN, Robert D.
 APPLICANT: WHITE, Owen R.
 APPLICANT: FRASER, Claire M.
 APPLICANT: VENTER, John C.
 TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 FILE REFERENCE: 24166-2007.00
 CURRENT APPLICATION NUMBER: US/09/103,840A
 CURRENT FILING DATE: 1998-06-24
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 4411529
 TYPE: DNA
 ORGANISM: Mycobacterium tuberculosis
 OTHER INFORMATION: H37Rv
 US-09-103-840A-1

Query Match Similarity 28.0%; Score 4586; DB 4; Length 4411529;
 Best Local Similarity 55.8%; Pred. No. 1-4e-123;
 Matches 875; Conservative 0; Mismatches 654; Indels 0; Gaps 0;

QY 1 ATGGCAAAAGAACATCAATTTCAGCAGATCGCGGTCTGCATGTTGCGGAGATGTGAT 60
 Db 528606 ATGGCCAAAGACATTCGCGACGAGAAGGCGCCGCTGCGGCCGCTGAC 528665
 QY 61 ATGTTAGCATACCTCAAGAACCTTGCTCTAAAGGGCGGAAGTTGTTCTGTAA 120
 Db 528666 GCCCCMCGGGAGTGGCTAAAGGGGACTGGCCCAAGGGCCGAAAGTCGCTCCGGAA 528725
 QY 121 AACGCTTGTGTCCTAATCTAATGACGGGGTAACTGCTAAAGAGTGTGAA 180
 Db 528726 AGAAAGTGGGGGCCCAAGAACACAGATGCTGCTCATGGCAGAGATCGAG 528785
 QY 181 TTATGAGATCATTTGAAACACGGGGCAANTGGTGTGAAGTGTCTAAACC 240
 Db 528786 CTGGAGGATTCGGCTTACAGAGAAGGGCGGAGGTGGCAAGAGGTGACAGAGAC 528845
 QY 241 ATGATATGCTGGGATGGGGATACAGCACACTTGTGACCAAGGCCATTCTCAT 300
 Db 528846 GATGAGCCGGGAGACGGCCACAGGGCTTACCGGCAACGGCTTACGGCTTACGG 528905
 QY 301 GAAAGCTAAATGAGTGCAGAGGTGCTAACTCAATTGTCTCGCGAGGCTGAA 360
 Db 528906 GAGGCCCTGGCAAGCTCGGGCGGCCAACCGCTCTCAAAAGCGCGCATCGA 528965
 QY 361 ACAGCAAGCACACAGCTGTGAGCTGAACGCCATTGTGACCTGATCTGAA 420
 Db 528966 AGGGCGCTGGGAGAAGTCACCGGCAACGGCTTACCGGCAAGGGCTTACGG 528985
 QY 421 GAAAGCTTGTGCTCAGGTGGAGATCTCACGGCTCTGAAGAATGAGTGTGATATC 480
 Db 529026 GAGCGAGATGGCCACCGCACGGATTGGCGGGTGGACAGCTGGTACCTGAC 529085
 QY 481 TCAGAGCTATGGCGGCTGGCAACGATGGTGTGTTACCATGAGAATCTGGAGT 540
 Db 529086 GCGCGGGCATGGCTCACCGGCAACGGGGTGGACCTGACCCGGCGCTG 529145

QY 561 AGGTTAAAGTCGACATCGAGCTTGCCACAGCTTGAGGAGCTTCTTAA 720
 Db 529266 GTCAGTCCTCAAGGTGTCGACTGTGCAAGATCTGATCTGCTGCGCTGAGAAGTCAC 780
 QY 721 ACCAACGGRCATATCTACTATATGCGAGATGTGGATGAGACTTCACCC 780
 Db 529205 TACTTGTGCGACGGCGCTGAGGCGCTCCGGAGGACCTCATCCGCG 529265
 QY 661 AGGTTAAAGTCGACATCGAGCTTGCCACAGCTTGAGGAGCTTCTTAA 720
 Db 529386 GTCGCGTCAAGAGTCGGGCCACCTGAGTCGCGGCTGAGCTCCACCC 780
 Db 529326 GCGGTAGCGCTGCTGAGCATCGCCGAGCTGAGGAGCTGAGCTGAGC 529385
 QY 781 GTCGCGACAAAGATTCGGTACTTCTGTCAGTGGTGTGTCAGAAGGCGGATTGTG 840
 Db 529446 GACCCCGCAAGGGATCGCGAGGATATGCCCTTCACGGGGTCAAGGCGC 529445
 QY 841 GATCGCTGCGTAAGCTGTGCTGAGCATGCTCTCTGAGAGTGGAGCTGAGT 900
 Db 529446 GACCCCGCAAGGGATCGCGAGGATATGCCCTTCACGGGGTCAAGGCGC 529505
 QY 901 GAGGATCTGAGCTGTGATAAAGATGCTACATGAGACGCGCTTGTGAGCT 960
 Db 529506 GAGGGGGGGCTGAGCTGCGTGGAGACCGCGACCTGTCGCTGCTGGAGGAGATCG 529565
 QY 961 ATGAGCTGAGAACATGACAGTATGCTGAGTGTGAGCTGAGCTGAGCT 1020
 Db 529566 GTCGCTGTCACCAAGGGAGACCATATGCGAGGGCGCGGGAGACCGAC 529625
 QY 1021 GCTAACCGTATGCTGAGCTGATTAATGCAATTGAAACACAACTCTGAC 1080
 Db 529626 GCGGGAGGAGTGGCCCAAGATCCGCCAGGAGATGGAGAC 529635
 QY 1081 GAAAACTCAAGAGCGTTGGGAATATTGCTGTTGTTGTTGTTAAAGTAGGA 1140
 Db 529686 GAGAGCTCAGGAGGCGTGGCAAGCTGCGGTGTCGGTATAGCCGGT 529745
 QY 1141 GTCGACACAGAGCACCTTAAAGAAATAAACCTGGCAATGAGGAGCT 1200
 Db 529746 GCGCCAACGGTGCACAGGGCGCAAGCACCGCACTGAGGAGTGGCTGC 529805
 QY 1201 ACACGTGCGCGTGTGAGAGGATATGCGTGTGTGTGAAAGCACTTATCGGT 1260
 Db 529806 GCGAACGGCGCCGCGTGGAGGGCAGTGGCGGGTGGGGTGTGACCTTGC 529865
 QY 1261 ATGAAAGTAGACGACCTCTGAGCTGGGGAGATGATGGGGTACATGG 1320
 Db 529866 GCCCCGACCCCTGAGGAGCTGGAGGAGCGACGGAGCGCGGCCAACATCGT 529925
 QY 1321 CTTCGTGCTCTGAGAGCTGACTCTAACATGCTTAAATGTTGGTAGAGCTC 1380
 Db 529926 AGGGGGCTGCTGAGCCCGCGTGGAGACATGCCCTACCGCTGGCTGAGCGCG 529985
 QY 1381 GTAGTGTATGAGCAAGTGGAAACAGCCCGCAGGAGCAAGGTTAATGCGCAACGGT 1440
 Db 529986 GTGGCGCCGAGAGGTGGCACCTGCGCGTGTGCGACGAGCTGAGCGCT 530045
 QY 1441 GAGTGGGTGATATGATTAACAGGAATCATGACCTCTCAAGAATGAC 1500
 Db 530046 GTCTTCAGGAGCTCTCTGCGCGTGTGCGACCGCTCAGGGTGGCG 530105
 QY 1501 CTTCAAATGCGCTCTCTGAGCTGAGCTGACAGAGGAGTGTGCTCAT 1560
 Db 530106 CTTCAGGAGTGGCTCATCGGGGCTGCTGACCCACGGGGCTG 530165
 QY 1561 AACCTGA 1569
 Db 530166 AACCGGAA 530174

